

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: FIDDES, J.C.
ABRAHAM, J.D.
- (ii) TITLE OF INVENTION: HUMAN BASIC FIBROBLAST GROWTH
FACTOR ANALOG
- (iii) NUMBER OF SEQUENCES: 69
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: MORRISON & FOERSTER
(B) STREET: 755 PAGE MILL ROAD
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304-1018
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: Windows
(D) SOFTWARE: FastSEQ for Windows Version 2.0b
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Lehnhardt, Susan K
(B) REGISTRATION NUMBER: 33,943
(C) REFERENCE/DOCKET NUMBER: 21900-20089.10
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 650-813-5600
(B) TELEFAX: 650-494-0792
(C) TELEX: 706141

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1969 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

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(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 970...1434
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AATTCATGCC	TCTTTCTCTC	CTTTTGTG	TGG TAGACGACTT	CAGCCTCTGT	CCTTTAATTT	60
TAAAGTTTAT	GCCCCACTTG	TACCCCTCGT	CTTTTGGTGA	TTTAGAGATT	TTCAAAGCCT	120
GCTCTGACAC	AGACTCTTCC	TTGGATTGCA	ACTTCTCTAC	TTTGGGGTGG	AAACGGCTTC	180
TCCGTTTTGA	AACGCTAGCG	GGGAAAAAAT	GGGGGAGAAA	GTGAGTTTA	AACTTTTAAA	240
AGTTGAGTCA	CGGCTGGTTG	CGCACGAAAA	GCCCCGCAGT	GTGGAGAAAG	CCTAAACGTG	300
GTTTGGGTGG	TGCGGGGGTT	GGGCGGGGGT	GACTTTTGGG	GGATAAGGGG	CGGTGGAGCC	360
CAGGGAATGC	CAAAGCCCTG	CCGCGGCCTC	CGACGCGCGC	CCCCCGCCCC	TCGCCTCTCC	420
CCCGCCCCCG	ACTGAGGCCG	GGCTCCCCGC	CGGACTGATG	TCGCGCGCTT	GCGTGTGTG	480
GCCGAAGCCG	CCGAAGCTAG	AGGCCGGCCC	CAGAAAACCC	GAGCGAGTAG	GGGGCGGCGC	540
GCAGGAGGGA	GGAGAACTGG	GGGCGCGGGA	GGCTGGTGGG	TGTGGGGGGT	GGAGATGTAG	600
AAGATGTGAC	GCCGCGGCCG	GGCGGGTGCC	AGATTAGCGG	ACGGCTGCCC	GCGGTTGCAA	660
CGGGATCCCG	GGCGCTGCAG	CTTGGGAGGC	GGCTCTCCCC	AGGCGGCGTC	CGCGGAGACA	720
CCCATCTGTG	AACCCACAGT	CCCGGGCCGC	CGGCTCGCCG	CGCACCAGGG	GCCGGCGGAC	780
AGAAGAGCGG	CCGAGCGGCT	CGAGGCTGGG	GGACCGCGGG	CGCGGCCGCG	CGCTGCCGGG	840
CGGGAGGCTG	GGGGGCCGGG	GCCGGGGCCG	TGCCCGGAGC	GGGTCGGAGG	CCGGGGCCGG	900
GGCCGGGGGA	CGGCGGCTCC	CCGCGCGGCT	CCAGCGGCTC	GGGGATCCCG	GCCGGGCCCC	960
GCAGGGACC	ATG GCA GCC	GGG AGC ATC	ACC ACG CTG	CCC GCC TTG	CCC GAG	1011
	Met Ala Ala	Gly Ser Ile	Thr Thr Leu	Pro Ala Leu	Pro Glu	
	1	5		10		
GAT GGC GGC	AGC GGC GCC	TTC CCG CCC	GGC CAC TTC	AAG GAC CCC	AAG	1059
Asp Gly Gly	Ser Gly Ala	Phe Pro Pro	Gly His Phe	Lys Asp Pro	Lys	
15	20		25	30		
CGG CTG TAC	TGC AAA AAC	GGG GGC TTC	TTC CTG CGC	ATC CAC CCC	GAC	1107
Arg Leu Tyr	Cys Lys Asn	Gly Gly Phe	Phe Leu Arg	Ile His Pro	Asp	
	35		40	45		
GGC CGA GTT	GAC GGG GTC	CGG GAG AAG	AGC GAC CCT	CAC ATC AAG	CTA	1155
Gly Arg Val	Asp Gly Val	Arg Glu Lys	Ser Asp Pro	His Ile Lys	Leu	
	50		55	60		
CAA CTT CAA	GCA GAA GAG	AGA GGA GTT	GTG TCT ATC	AAA GGA GTG	TGT	1203
Gln Leu Gln	Ala Glu Glu	Arg Gly Val	Val Ser Ile	Lys Gly Val	Cys	
	65		70	75		
GCT AAC CGT	TAC CTG GCT	ATG AAG GAA	GAT GGA AGA	TTA CTG GCT	TCT	1251
Ala Asn Arg	Tyr Leu Ala	Met Lys Glu	Asp Gly Arg	Leu Leu Ala	Ser	
	80		85	90		
AAA TGT GTT	ACG GAT GAG	TGT TTC TTT	TTT GAA CGA	TTG GAA TCT	AAT	1299
Lys Cys Val	Thr Asp Glu	Cys Phe Phe	Phe Glu Arg	Leu Glu Ser	Asn	
95	100		105	110		
AAC TAC AAT	ACT TAC CGG	TCA AGG AAA	TAC ACC AGT	TGG TAT GTG	GCA	1347
Asn Tyr Asn	Thr Tyr Arg	Ser Arg Lys	Tyr Thr Ser	Trp Tyr Val	Ala	
	115		120	125		

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TTG AAA CGA ACT GGG CAG TAT AAA CTT GGA TCC AAA ACA GGA CCT GGG 1395
 Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly
 130 135 140

CAG AAA GCT ATA CTT TTT CTT CCA ATG TCT GCT AAG AGC TGATTTTAAT GG 1446
 Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser
 145 150 155

CCACATCTAA TCTCATTTCA CATGAAAGAA GAAGTATATT TTAGAAATTT GTTAATGAGA 1506
 GTAAAAGAAA ATAAATGTGT ATAGCTCAGT TTGGATAATT GGTCAAACAA TTTTTTATCC 1566
 AGTAGTAAAA TATGTAACCA TGCCCAGTAA AGAAAAATAA CAAAAGTTGT AAAATGTATA 1626
 TTCTCCCTTT TATATTGCAT CTGCTGTTAC CCAGTGAAGC TTACCTAGAG CAATGATCTT 1686
 TTTACGCAT TTGCTTTATT CGAAAAGAGG CTTTTAAAT GTGCATGTTT AGAAAACAAA 1746
 ATTTCTTCAT GGAAATCATA TACATTAGAA AATCACAGTC AGATGTTTAA TCAATCCAAA 1806
 AATGTCCACT ATTTCTTATG TCATTCGTTA GTCTACATGT TTCTAAACAT ATAAATGTGA 1866
 ATTTAATCAA TTCCTTTCAT AGTTTTATAA TTCTCTGGCA GTTCCTTATG ATAGAGTTTA 1926
 TAAACAGTC CTGTGTAAAC TGCTGGAAGT TCTCCGGAA TTC 1969

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu Asp Gly
 1 5 10 15
 Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys Arg Leu
 20 25 30
 Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp Gly Arg
 35 40 45
 Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu Gln Leu
 50 55 60
 Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys Ala Asn
 65 70 75 80
 Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser Lys Cys
 85 90 95
 Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn Asn Tyr
 100 105 110
 Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala Leu Lys
 115 120 125
 Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly Gln Lys
 130 135 140
 Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser
 145 150 155

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 638 base pairs
- (B) TYPE: nucleic acid

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(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA
(ix) FEATURE:

(A) NAME/KEY: Coding Sequence
(B) LOCATION: 91...555
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TGCATTTTGT	GCCTTTGCTG	GAAGAACCGA	CTACAGGTTT	GTTCAATTTC	TTACAGTCTT	60
GAAAGCGCCA	CAAGCAGCAG	CTGCTGAGCC	ATG GCT GAA	GGG GAA ATC	ACC ACC	114
	Met	Ala	Glu	Gly	Glu Ile Thr Thr	
	1			5		
TTC ACA GCC	CTG ACC GAG	AAG TTT AAT	CTG CCT CCA	GGG AAT TAC	AAG	162
Phe Thr Ala	Leu Thr Glu	Lys Phe Asn	Leu Pro Pro	Gly Asn Tyr	Lys	
10		15		20		
AAG CCC AAA	CTC CTC TAC	TGT AGC AAC	GGG GGC CAC	TTC CTG AGG	ATC	210
Lys Pro Lys	Leu Leu Tyr	Cys Ser Asn	Gly Gly His	Phe Leu Arg	Ile	
25		30		35	40	
CTT CCG GAT	GGC ACA GTG	GAT GGG ACA	AGG GAC AGG	AGC GAC CAG	CAC	258
Leu Pro Asp	Gly Thr Val	Asp Gly Thr	Arg Asp Arg	Ser Asp Gln	His	
	45		50		55	
ATT CAG CTG	CAG CTC AGT	GCG GAA AGC	GTG GGG GAG	GTG TAT ATA	AAG	306
Ile Gln Leu	Gln Leu Ser	Ala Glu Ser	Val Gly Glu	Val Tyr Ile	Lys	
	60		65		70	
AGT ACC GAG	ACT GGC CAG	TAC TTG GCC	ATG GAC ACC	GAC GGG CTT	TTA	354
Ser Thr Glu	Thr Gly Gln	Tyr Leu Ala	Met Asp Thr	Asp Gly Leu	Leu	
	75		80		85	
TAC GGC TCA	CAG ACA CCA	AAT GAG GAA	TGT TTG TTC	CTG GAA AGG	CTG	402
Tyr Gly Ser	Gln Thr Pro	Asn Glu Glu	Cys Leu Phe	Leu Glu Arg	Leu	
90		95		100		
GAG GAG AAC	CAT TAC AAC	ACC TAT ATA	TCC AAG AAG	CAT GCA GAG	AAG	450
Glu Glu Asn	His Tyr Asn	Thr Tyr Ile	Ser Lys Lys	His Ala Glu	Lys	
105		110		115	120	
AAT TGG TTT	GTT GGC CTC	AAG AAG AAT	GGG AGC TGC	AAA CGC GGT	CCT	498
Asn Trp Phe	Val Gly Leu	Lys Lys Asn	Gly Ser Cys	Lys Arg Gly	Pro	
	125		130		135	
CGG ACT CAC	TAT GGC CAG	AAA GCA ATC	TTG TTT CTC	CCC CTG CCA	GTC	546
Arg Thr His	Tyr Gly Gln	Lys Ala Ile	Leu Phe Leu	Pro Leu Pro	Val	
	140		145		150	
TCT TCT GAT	TAAAGAGATC	TGTTCTGGGT	GTTGACCACT	CCAGAGAAGT	TTCGAGGGG	604
Ser Ser Asp						
155						

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TCCTCACCTG GTTGACCCAA AAATGTTCCC TTGA

638

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 155 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Ala Glu Gly Glu Ile Thr Thr Phe Thr Ala Leu Thr Glu Lys Phe
 1 5 10 15
 Asn Leu Pro Pro Gly Asn Tyr Lys Lys Pro Lys Leu Leu Tyr Cys Ser
 20 25 30
 Asn Gly Gly His Phe Leu Arg Ile Leu Pro Asp Gly Thr Val Asp Gly
 35 40 45
 Thr Arg Asp Arg Ser Asp Gln His Ile Gln Leu Gln Leu Ser Ala Glu
 50 55 60
 Ser Val Gly Glu Val Tyr Ile Lys Ser Thr Glu Thr Gly Gln Tyr Leu
 65 70 75 80
 Ala Met Asp Thr Asp Gly Leu Leu Tyr Gly Ser Gln Thr Pro Asn Glu
 85 90 95
 Glu Cys Leu Phe Leu Glu Arg Leu Glu Glu Asn His Tyr Asn Thr Tyr
 100 105 110
 Ile Ser Lys Lys His Ala Glu Lys Asn Trp Phe Val Gly Leu Lys Lys
 115 120 125
 Asn Gly Ser Cys Lys Arg Gly Pro Arg Thr His Tyr Gly Gln Lys Ala
 130 135 140
 Ile Leu Phe Leu Pro Leu Pro Val Ser Ser Asp
 145 150 155

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGAATTCAAA TATTCTGAAA TGAGCTGTTG ACAATTAATC ATCGAACTAG TTAAC TAGTA 60
 CGCAAGTTCA CGTAAAAAGG GTATCACATA TGGTACCTGC AGA 103

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TCTGCAGGTA CCATATGTGA TACCCTTTTT ACGTGAAC TT GCGTACTAGT TAACTAGTTC 60
GATGATTAAT TGTCAACAGC TCATTTT CAGA ATATTTGAAT TCT 103

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GAAATACACC AGTTGG 16

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ACTTGATCC AAAACAG 17

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTTTACATGA AGCTTTATAT TTCAG 25

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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32

28

28

28

19

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TAGAACCAGC AGCCATATGA

20

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TCTTCTGGCA GAGCTGGCAG GGTAGTGA

--28--

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ACCTGGTGGG AAGGCACCAG AACCACCG

28

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

AGTACAGACG TTTTGGGTCT TTGAAGTG

28

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AGCTTGCGCA GGAAGAAACC ACCGTTTTTG C

31

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

AGCTTCATAT GGCTGCTGGT TCTATCACTA CCCTGCCAGC TCTGCCAGAA GACGGTGGTT	60
CTGGTGCCTT CCCACCAGGT CACTTCAAAG ACCCAAAACG TCTGTACTGC AAAAACGGTG	120
GTTTCTTCCT GCGCA	135

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

AGCTTGCGCA GGAAGAAACC ACCGTTTTTG CAGTACAGAC GTTTTGGGTC TTTGAAGTGA	60
CCTGGTGGGA AGGCACCAGA ACCACCGTCT TCTGGCAGAG CTGGCAGGGT AGTGATAGAA	120
CCAGCAGCCA TATGA	135

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

ACGTCTGTAC TCCAAAAACG GTG

23

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TACAGACGAG TCTTTCTTTT TTG

23

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CAAAGGAGTG TCTGCAAACC GTT

23

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

AGCTTCTAAA TCTGTTACAG ACG

23

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ACGTCTGTAC TCCAAAAACG GTG

23

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TACAGACGAG TCTTTCTTTT TTG

23

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GTCTGTACTG CTCAAACGGT GGTT

24

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

TTTCTTCCTG CTCATCCACC CCG

23

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CATCCACCCC GCCGGCCGAG TGG

23

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CCCCGACGGC CTAGTGGACG GGG

23

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(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

ACCCCGACGG CGCAGTGGAC GGGG

24

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CGGCCGGAGT GGCCGGGGTC CGCG

--- 24 ---

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GAGTGGACGG GAAACGCGAG AAGAG

25

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGACGGGGTC CTCGAGAAGA GCG

23

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GGTCCGCGAG ATGAGCGACC CAC

23

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGTCCGCGAG ATAAGCGACC CACA

24

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CGAGAAGAGC GCCCCACACA TCA

23

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GAGCGACCCA AACATCAAAC TAC

23

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

AGAAGATGGA ACTTTACTAG CTTC

24

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ATGTGTTACA GCAGAGTGT TCT

23

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GTTACAGACG CCTGTTTCTT TTTTG

25

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

GTGTTACAGA CAGTTGTTTC TTTTT

25

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GTTTCTTTTT TTCACGATTG GAGT

24

T06020"09420660

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CTTTTTTGAA CTATTGGAGT CTA

23

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

TGAACGATTG GCATCTAATA ACTA

24

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

AGTCTAATAA CGCAAATACT TACCG

25

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CTAATAACTA CAGTACTTAC CGG

23

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid

0906460-070901

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CAATACTTAC ACTTCAAGGA AATA

24

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

CAATACTTAC CTGTCAAGGA AAT

23

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

ACCGGTCAAG GTCTTACACC AGTTG

25

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

GGTGGTTTCT TCCACCCCGA CGGC

24

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

T06020-0942000

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CCCGACGGCC GAGTCCGCGA GAAG

24

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

CCACACATCA AACAAGCAGA AGAG

24

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

GCAAACCGTT ACAAAGAAGA TGGA

24

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

TGTTTCTTTT TTGAGTCTAA TAAC

24

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

GAGTCTAATA ACTACCGGTC AAGG

24

0990450-09720560

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

AGGTCAC TTC ATGGACCCAA AACG

24

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

TCAAAGACCC AGCACGTCTG TACT

24

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

AAGACCCAAA ATCTCTGTAC TGCA

24

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

GTCACTTCAA AAAGCCAAAA CGTCT

25

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid

T06520-09420650

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

23

(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

24

(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25

(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

25

(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GGCACTGAAA ACTACTGGGC AGT

23

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

CTGGGCAGTA TTCTCTTGGA TCCAA

25

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

AACTTGGATC CTCTACAGGA CCTGG

25

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

TTGGGTCTTT GAAGTGCATA TGTGGGAAGG CACCAG

36

09902460-070901